# Transcription Factor LjWRKY50 Affects Jasmonate-Regulated Floral Bud Duration in *Lonicera japonica*

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**Supplemental Figure legend**

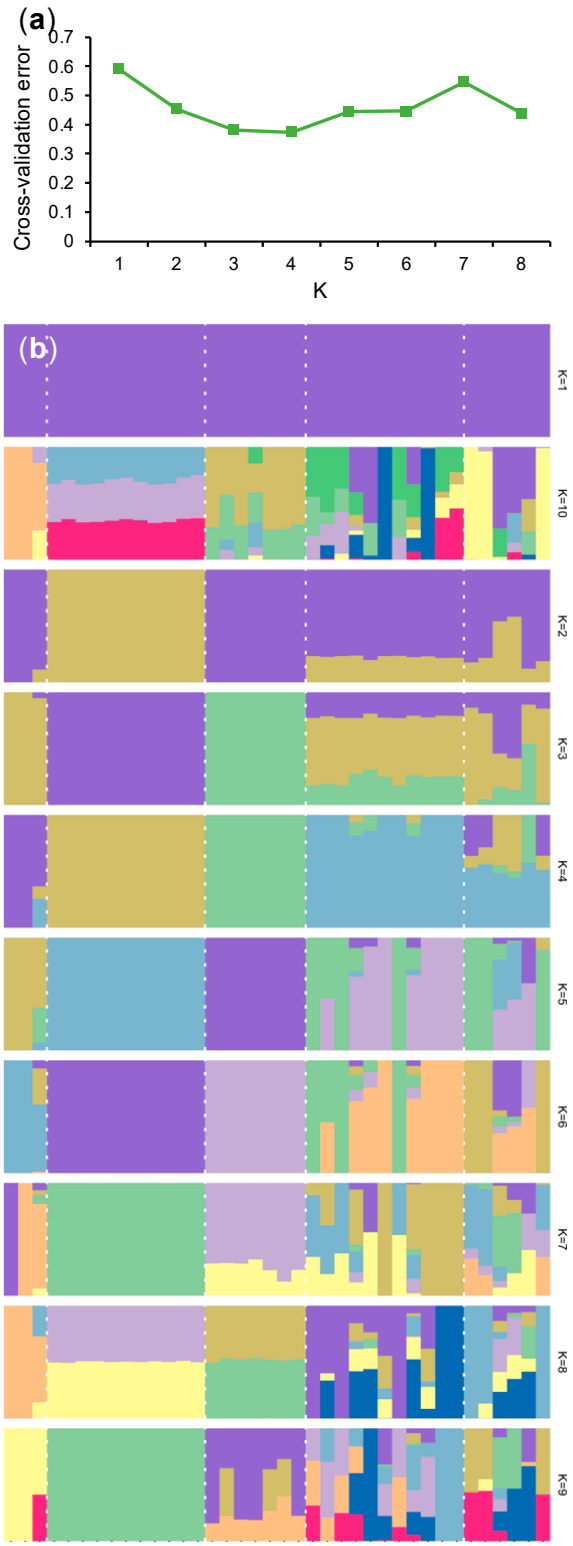


**Figure S1** Population structure analysis of 38 Lonicera samples using ADMIXTURE software. (**a**) The cross-validation error from ADMIXTURE software; (**b**) Population

structure from clusters one to ten. Each color and bar represents an individual population and accession, respectively. The segments of different colors represent the proportions of ancestral populations. A dashed white line divides the accessions into five distinct clusters.

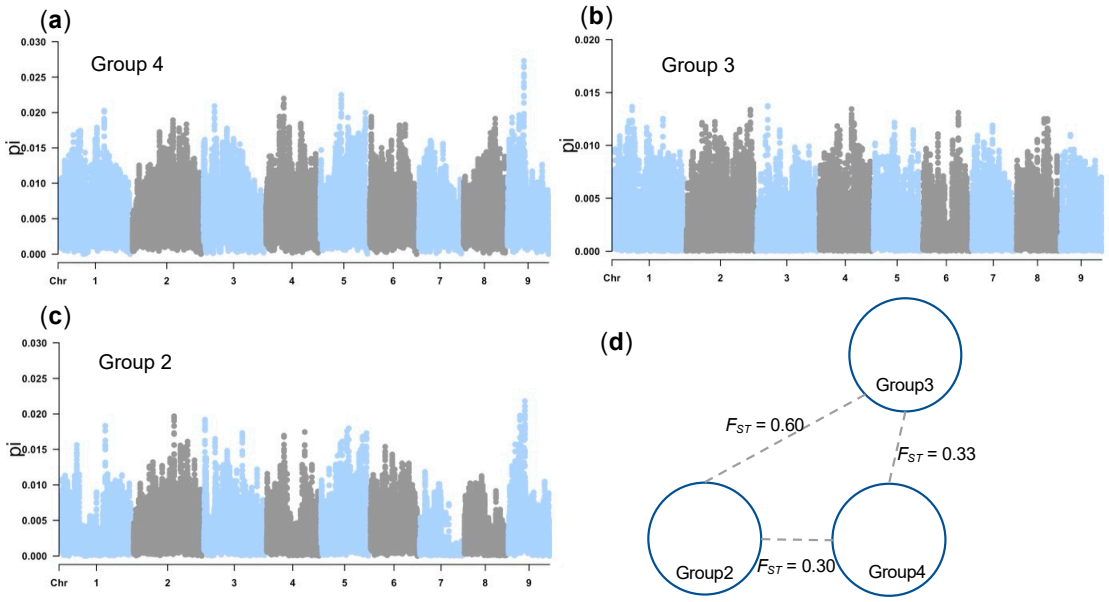


**Figure S2** The nucleotide diversity (π) analyses using 35 resequenced *L. japonica* germplasms. (**a-c**) The Manhattan plots display the nucleotide diversity (π) of Group 4, Group 3, and Group 2 across the entire genome, employing a 100 kb window and a 10 kb step, respectively; (**d**) The average nucleotide diversity (π) within the group.

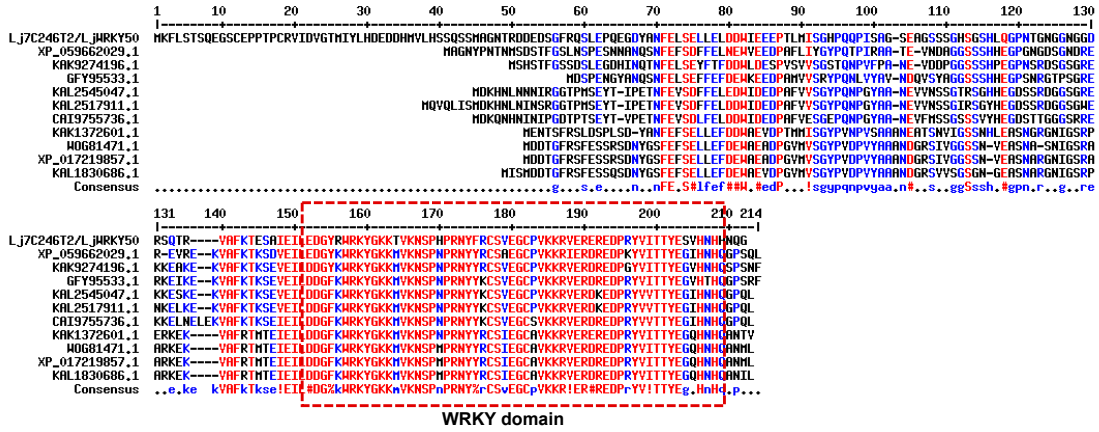


**Figure S3** The alignment results of the putative protein sequence for WRKY50 in *L. japonica* and the other ten species.

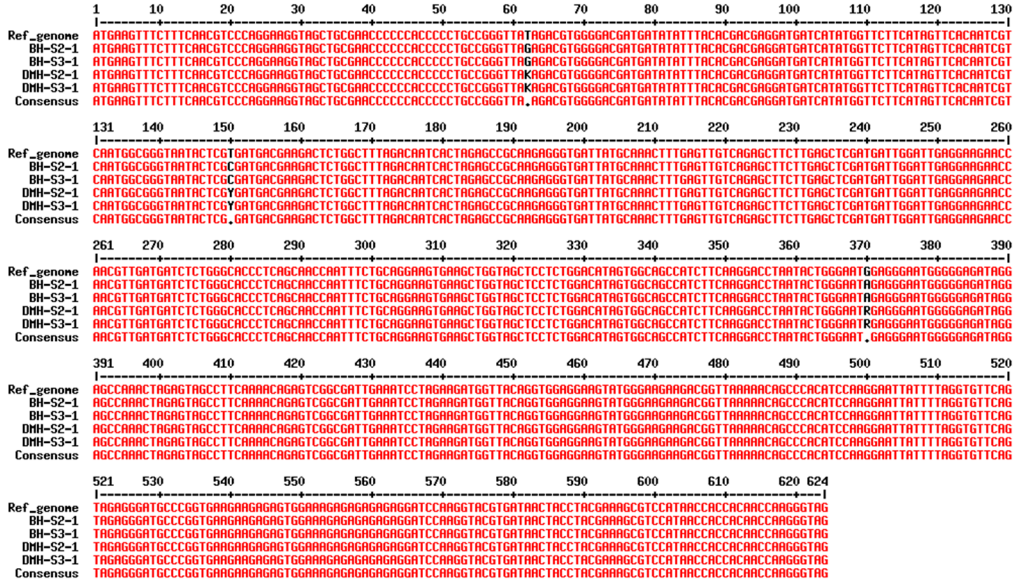


**Figure S4** The alignment of CDS sequences for the LjWRKY50 gene, which was cloned from the long- and short-duration floral bud varieties BH and DMH, involved two biological replications.